

GEPHE SUMMARY

	Gephebase Gene		GepheID
Zmr1 ( <a href="https://www.gephebase.org/search-criteria?/and+GeneGephebase=^Zmr1^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+GeneGephebase=^Zmr1^#gephebase-summary-title</a> )		GP00001715	
	Entry Status	Courtier	Main curator
Published			

PHENOTYPIC CHANGE

Trait #1	Trait Category
Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+TraitCategory=^Physiology^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+TraitCategory=^Physiology^#gephebase-summary-title</a> )	Trait
Xenobiotic resistance (fungicide) ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic resistance (fungicide)^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic resistance (fungicide)^#gephebase-summary-title</a> )	Trait State in Taxon A
high melanin levels - lower growth rate in absence of fungicide - higher growth rate in presence of fungicide	Trait State in Taxon B
low melanin levels - higher growth rate in absence of fungicide	

Trait #2	Trait Category
Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+TraitCategory=^Physiology^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+TraitCategory=^Physiology^#gephebase-summary-title</a> )	Trait
Melanin content ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=^Melanin content^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait=^Melanin content^#gephebase-summary-title</a> )	Trait State in Taxon A
high melanin levels - lower growth rate in absence of fungicide - higher growth rate in presence of fungicide	Trait State in Taxon B
low melanin levels - higher growth rate in absence of fungicide	

	Ancestral State		
Data not curated		Taxonomic Status	
Intraspecific ( <a href="https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=^Intraspecific^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=^Intraspecific^#gephebase-summary-title</a> )			
	Taxon A		Taxon B
	Latin Name		Latin Name
Zymoseptoria tritici ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Zymoseptoria tritici^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Zymoseptoria tritici^#gephebase-summary-title</a> )		Zymoseptoria tritici ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Zymoseptoria tritici^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Zymoseptoria tritici^#gephebase-summary-title</a> )	
-	Common Name	-	Common Name
	Synonyms		Synonyms
Zymoseptoria tritici (Desm.) Quaedvlieg & Crous 2011; CBS 115943; CBS:115943; IPO 323; IPO:323		Zymoseptoria tritici (Desm.) Quaedvlieg & Crous 2011; CBS 115943; CBS:115943; IPO 323; IPO:323	
species	Rank	species	Rank
	Lineage		Lineage
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Pezizomycotina; leotiomyceta; dothideomyceta; Dothideomycetes; Dothideomycetidae; Capnodiales; Mycosphaerellaceae; Zymoseptoria		cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Pezizomycotina; leotiomyceta; dothideomyceta; Dothideomycetes; Dothideomycetidae; Capnodiales; Mycosphaerellaceae; Zymoseptoria	
	Parent		Parent
Zymoseptoria () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1047167">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1047167</a> )		Zymoseptoria () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1047167">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1047167</a> )	
1047171 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1047171">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1047171</a> )	NCBI Taxonomy ID	1047171 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1047171">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1047171</a> )	NCBI Taxonomy ID
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
Yes		Yes	
	Taxon A Description		Taxon B Description
strain 3D7		strain 3D1	

GENOTYPIC CHANGE

CMR1	Generic Gene Name	UniProtKB Cochliobolus heterostrophus
		Q06F33 ( <a href="http://www.uniprot.org/uniprot/Q06F33">http://www.uniprot.org/uniprot/Q06F33</a> )
	Synonyms	GenebankID or UniProtKB
	String	0
-		
-		
-	Sequence Similarities	
GO - Molecular Function		
GO:0008270 : zinc ion binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0008270">https://www.ebi.ac.uk/QuickGO/term/GO:0008270</a> )		
GO:0003677 : DNA binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0003677">https://www.ebi.ac.uk/QuickGO/term/GO:0003677</a> )		
GO:0000981 : DNA-binding transcription factor activity, RNA polymerase II-specific ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0000981">https://www.ebi.ac.uk/QuickGO/term/GO:0000981</a> )		
GO - Biological Process		
GO:0006351 : transcription, DNA-templated ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0006351">https://www.ebi.ac.uk/QuickGO/term/GO:0006351</a> )		
GO - Cellular Component		
GO:0005634 : nucleus ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005634">https://www.ebi.ac.uk/QuickGO/term/GO:0005634</a> )		
Mutation #1		Presumptive Null
No ( <a href="https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title</a> )		Molecular Type
Cis-regulatory ( <a href="https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title</a> )		Aberration Type
Insertion ( <a href="https://www.gephebase.org/search-criteria?/and+Aberration Type=^Insertion^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Aberration Type=^Insertion^#gephebase-summary-title</a> )		Insertion Size
10-100 kb		Molecular Details of the Mutation
insertion of a transposable element island (13 TE interspersed by simple repeats) of approximately 30 kb, located 1862 bp upstream of Zmr1 start codon - analysis of knock out lines of the TE island insertion		Experimental Evidence
Linkage Mapping ( <a href="https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title</a> )		Main Reference
Transposable element insertions shape gene regulation and melanin production in a fungal pathogen of wheat. (2018) ( <a href="https://pubmed.ncbi.nlm.nih.gov/30012138">https://pubmed.ncbi.nlm.nih.gov/30012138</a> )		Authors
Krishnan P; Meile L; Plissonneau C; Ma X; Hartmann FE; Croll D; McDonald BA; SÄınchez-Vallet A		Abstract
Fungal plant pathogens pose major threats to crop yield and sustainable food production if they are highly adapted to their host and the local environment. Variation in gene expression contributes to phenotypic diversity within fungal species and affects adaptation. However, very few cases of adaptive regulatory changes have been reported in fungi and the underlying mechanisms remain largely unexplored. Fungal pathogen genomes are highly plastic and harbor numerous insertions of transposable elements, which can potentially contribute to gene expression regulation. In this work, we elucidated how transposable elements contribute to variation in melanin accumulation, a quantitative trait in fungi that affects survival under stressful conditions.		
We demonstrated that differential transcriptional regulation of the gene encoding the transcription factor Zmr1, which controls expression of the genes in the melanin biosynthetic gene cluster, is responsible for variation in melanin accumulation in the fungal plant pathogen Zymoseptoria tritici. We show that differences in melanin levels between two strains of Z. tritici are due to two levels of transcriptional regulation: (1) variation in the promoter sequence of Zmr1 and (2) an insertion of transposable elements upstream of the Zmr1 promoter. Remarkably, independent insertions of transposable elements upstream of Zmr1 occurred in 9% of Z. tritici strains from around the world and negatively regulated Zmr1 expression, contributing to variation in melanin accumulation.		
Our studies identified two levels of transcriptional control that regulate the synthesis of melanin. We propose that these regulatory mechanisms evolved to balance the fitness costs associated with melanin production against its positive contribution to survival in stressful environments.		Additional References

Mutation #2	
No ( <a href="https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title</a> )	Presumptive Null
Cis-regulatory ( <a href="https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title</a> )	Molecular Type
SNP ( <a href="https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title</a> )	Aberration Type
several candidate SNP - tests using reporter transgenes	Molecular Details of the Mutation
Linkage Mapping ( <a href="https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title</a> )	Experimental Evidence
Transposable element insertions shape gene regulation and melanin production in a fungal pathogen of wheat. (2018) ( <a href="https://pubmed.ncbi.nlm.nih.gov/30012138">https://pubmed.ncbi.nlm.nih.gov/30012138</a> )	Main Reference
Krishnan P; Meile L; Plissonneau C; Ma X; Hartmann FE; Croll D; McDonald BA; SÄınchez-Vallet A	Authors
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stressful conditions.

We demonstrated that differential transcriptional regulation of the gene encoding the transcription factor Zmr1, which controls expression of the genes in the melanin biosynthetic gene cluster, is responsible for variation in melanin accumulation in the fungal plant pathogen *Zymoseptoria tritici*. We show that differences in melanin levels between two strains of *Z. tritici* are due to two levels of transcriptional regulation: (1) variation in the promoter sequence of Zmr1 and (2) an insertion of transposable elements upstream of the Zmr1 promoter. Remarkably, independent insertions of transposable elements upstream of Zmr1 occurred in 9% of *Z. tritici* strains from around the world and negatively regulated Zmr1 expression, contributing to variation in melanin accumulation.

Our studies identified two levels of transcriptional control that regulate the synthesis of melanin. We propose that these regulatory mechanisms evolved to balance the fitness costs associated with melanin production against its positive contribution to survival in stressful environments.

Additional References

RELATED GEPHE

	Related Genes
No matches found.	
	Related Haplotypes
No matches found.	

EXTERNAL LINKS

COMMENTS

@TE ; check for UniProtKB and orthology with Cmr1